



## SEQUENCE LISTING

<110> Kahn, C. Ronald  
Zhu, Jianhua

<120> MODULATING THE RAD-NM23 INTERACTION

<130> 10276-017002

<140> US 10/074,694

<141> 2002-02-12

<150> US 09/053,967

<151> 1998-04-02

<160> 5

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 308

<212> PRT

<213> Homo sapiens

<400> 1

Met	Thr	Leu	Asn	Gly	Gly	Gly	Ser	Gly	Ala	Gly	Gly	Ser	Arg	Gly	Gly		
1				5					10					15			
Gly	Gln	Glu	Arg	Glu	Arg	Arg	Arg	Gly	Ser	Thr	Pro	Trp	Gly	Pro	Ala		
			20					25					30				
Pro	Pro	Leu	His	Arg	Arg	Ser	Met	Pro	Val	Asp	Glu	Arg	Asp	Leu	Gln		
		35				40					45						
Ala	Ala	Leu	Thr	Pro	Gly	Ala	Leu	Thr	Ala	Ala	Ala	Ala	Gly	Thr	Gly		
	50					55					60						
Thr	Gln	Gly	Pro	Arg	Leu	Asp	Trp	Pro	Glu	Asp	Ser	Glu	Asp	Ser	Leu		
65					70				75					80			
Ser	Ser	Gly	Gly	Ser	Asp	Ser	Asp	Glu	Ser	Val	Tyr	Lys	Val	Leu	Leu		
			85					90					95				
Leu	Gly	Ala	Pro	Gly	Val	Gly	Lys	Ser	Ala	Leu	Ala	Arg	Ile	Phe	Gly		
		100						105					110				
Gly	Val	Glu	Asp	Gly	Pro	Glu	Ala	Glu	Ala	Ala	Gly	His	Thr	Tyr	Asp		
		115					120					125					
Arg	Ser	Ile	Val	Val	Asp	Gly	Glu	Glu	Ala	Ser	Leu	Met	Val	Tyr	Asp		
	130					135					140						
Ile	Trp	Glu	Gln	Asp	Gly	Gly	Arg	Trp	Leu	Pro	Gly	His	Cys	Met	Ala		
145				150					155					160			
Met	Gly	Asp	Ala	Tyr	Val	Ile	Val	Tyr	Ser	Val	Thr	Asp	Lys	Gly	Ser		
			165						170					175			
Phe	Glu	Lys	Ala	Ser	Glu	Leu	Arg	Val	Gln	Leu	Arg	Arg	Ala	Arg	Gln		
		180						185					190				
Thr	Asp	Asp	Val	Pro	Ile	Ile	Leu	Val	Gly	Asn	Lys	Ser	Asp	Leu	Val		
	195						200					205					
Arg	Ser	Arg	Glu	Val	Ser	Val	Asp	Glu	Gly	Arg	Ala	Cys	Ala	Val	Val		
	210					215					220						
Phe	Asp	Cys	Lys	Phe	Ile	Glu	Thr	Ser	Ala	Ala	Leu	His	His	Asn	Val		
225					230						235				240		

```
<220>  
<221> CDS  
<222> (1) ... (498)
```

<400> 2																	
cag	tcg	cag	ccg	gcg	gta	aag	cct	tgt	cat	ctg	aag	ggg	acc	atg	gcc	48	
Gln	Ser	Gln	Pro	Ala	Val	Lys	Pro	Cys	His	Leu	Lys	Gly	Thr	Met	Ala		
1				5					10					15			
aac	agt	gag	cgt	acc	ttc	att	gcc	atc	aag	cct	gat	ggg	gtc	cag	cgg	96	
Asn	Ser	Glu	Arg	Thr	Phe	Ile	Ala	Ile	Lys	Pro	Asp	Gly	Val	Gln	Arg		
			20					25					30				
ggg	ctg	gtg	ggc	gag	atc	atc	aag	cgg	ttc	gag	cag	aag	ggg	ttc	cgc	144	
Gly	Leu	Val	Gly	Glu	Ile	Ile	Lys	Arg	Phe	Glu	Gln	Lys	Gly	Phe	Arg		
		35					40					45					
ctt	gtt	ggt	ctg	aag	ttt	ctg	cag	gct	tca	gag	gac	ctt	ctc	aag	gag	192	
Leu	Val	Gly	Leu	Lys	Phe	Leu	Gln	Ala	Ser	Glu	Asp	Leu	Leu	Lys	Glu		
	50					55					60						
cac	tac	act	gac	ctg	aag	gac	cgc	ccc	ttc	ttt	act	ggc	ctg	gtg	aaa	240	
His	Tyr	Thr	Asp	Leu	Lys	Asp	Arg	Pro	Phe	Phe	Thr	Gly	Leu	Val	Lys		
65					70				75						80		
tac	atg	cac	tca	gga	cca	gtg	gtt	gct	atg	gtc	tgg	gag	ggt	ctg	aat	288	
Tyr	Met	His	Ser	Gly	Pro	Val	Val	Ala	Met	Val	Trp	Glu	Gly	Leu	Asn		
			85					90						95			
gtg	gtg	aag	aca	ggc	cgc	gtg	atg	ctt	gga	gag	acc	aac	ccc	gca	gac	336	
Val	Val	Lys	Thr	Gly	Arg	Val	Met	Leu	Gly	Glu	Thr	Asn	Pro	Ala	Asp		
			100					105					110				
tct	aag	cct	ggg	acc	ata	cga	gga	gac	ttc	tgc	att	caa	gtt	ggc	agg	384	
Ser	Lys	Pro	Gly	Thr	Ile	Arg	Gly	Asp	Phe	Cys	Ile	Gln	Val	Gly	Arg		
		115					120					125					
aac	atc	att	cat	ggc	agc	gat	tct	gta	aag	agc	gca	gag	aag	gag	atc	432	
Asn	Ile	Ile	His	Gly	Ser	Asp	Ser	Val	Lys	Ser	Ala	Glu	Lys	Glu	Ile		
130						135					140						

agc ttg tgg ttt cag cct gag gag ctg gtg gag tac aag agc tgt gcg 480  
 Ser Leu Trp Phe Gln Pro Glu Glu Leu Val Glu Tyr Lys Ser Cys Ala  
 145 150 155 160

cag aac tgg atc tat gag tgataggacg gtgccggttt tctacctgct 528  
 Gln Asn Trp Ile Tyr Glu  
 165

tactcttgtt ctcacaggca ggggaccagc aaccctagat atttctggaa cttctttgac 588  
 ctggaaggaa cctttgggag ccgtgactcc ctgtgcagtg ttacgtgccca ctggttagatt 648  
 aaagtgttta atctgt 664

<210> 3  
 <211> 166  
 <212> PRT  
 <213> Mus musculus

<400> 3  
 Gln Ser Gln Pro Ala Val Lys Pro Cys His Leu Lys Gly Thr Met Ala  
 1 5 10 15  
 Asn Ser Glu Arg Thr Phe Ile Ala Ile Lys Pro Asp Gly Val Gln Arg  
 20 25 30  
 Gly Leu Val Gly Glu Ile Ile Lys Arg Phe Glu Gln Lys Gly Phe Arg  
 35 40 45  
 Leu Val Gly Leu Lys Phe Leu Gln Ala Ser Glu Asp Leu Leu Lys Glu  
 50 55 60  
 His Tyr Thr Asp Leu Lys Asp Arg Pro Phe Phe Thr Gly Leu Val Lys  
 65 70 75 80  
 Tyr Met His Ser Gly Pro Val Val Ala Met Val Trp Glu Gly Leu Asn  
 85 90 95  
 Val Val Lys Thr Gly Arg Val Met Leu Gly Glu Thr Asn Pro Ala Asp  
 100 105 110  
 Ser Lys Pro Gly Thr Ile Arg Gly Asp Phe Cys Ile Gln Val Gly Arg  
 115 120 125  
 Asn Ile Ile His Gly Ser Asp Ser Val Lys Ser Ala Glu Lys Glu Ile  
 130 135 140  
 Ser Leu Trp Phe Gln Pro Glu Glu Leu Val Glu Tyr Lys Ser Cys Ala  
 145 150 155 160  
 Gln Asn Trp Ile Tyr Glu  
 165

<210> 4  
 <211> 670  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (73)...(528)

<400> 4  
 cggccacgag gcggaatccc ttctgctctc ccagcgcagc gccgccgccc ggccccctcca 60  
 gcttcccggga cc atg gcc aac ctg gag cgc acc ttc atc gcc atc aag ccg 111  
 Met Ala Asn Leu Glu Arg Thr Phe Ile Ala Ile Lys Pro  
 1 5 10

gac ggc gtg cag cgc ggc ctg gtg ggc gag atc atc aag cgc ttc gag 159  
 Asp Gly Val Gln Arg Gly Leu Val Gly Glu Ile Ile Lys Arg Phe Glu  
 15 20 25  
 cag aag gga ttc cgc ctc gtg gcc atg aag ttc ctc cgg gcc tct gaa 207  
 Gln Lys Gly Phe Arg Leu Val Ala Met Lys Phe Leu Arg Ala Ser Glu  
 30 35 40 45  
 gaa cac ctg aag cag cac tac att gac ctg aaa gac cga cca ttc ttc 255  
 Glu His Leu Lys Gln His Tyr Ile Asp Leu Lys Asp Arg Pro Phe Phe  
 50 55 60  
 cct ggg ctg gtg aag tac atg aac tca ggg ccg gtt gtg gcc atg gtc 303  
 Pro Gly Leu Val Lys Tyr Met Asn Ser Gly Pro Val Val Ala Met Val  
 65 70 75  
 tgg gag ggg ctg aac gtg gtg aag aca ggc cga gtg atg ctt ggg gag 351  
 Trp Glu Gly Leu Asn Val Val Lys Thr Gly Arg Val Met Leu Gly Glu  
 80 85 90  
 acc aat cca gca gat tca aag cca ggc acc att cgt ggg gac ttc tgc 399  
 Thr Asn Pro Ala Asp Ser Lys Pro Gly Thr Ile Arg Gly Asp Phe Cys  
 95 100 105  
 att cag gtt ggc agg aac atc att cat ggc agt gat tca gta aaa agt 447  
 Ile Gln Val Gly Arg Asn Ile Ile His Gly Ser Asp Ser Val Lys Ser  
 110 115 120 125  
 gct gaa aaa gaa atc agc cta tgg ttt aag cct gaa gaa ctg gtt gac 495  
 Ala Glu Lys Glu Ile Ser Leu Trp Phe Lys Pro Glu Glu Leu Val Asp  
 130 135 140  
 tac aag tct tgt gct cat gac tgg gtc tat gaa taagaggtgg acacaacagc 548  
 Tyr Lys Ser Cys Ala His Asp Trp Val Tyr Glu  
 145 150  
 agtctccttc agcacggcgt ggtgtgtccc tggacacagc tcttcattcc attgacttag 608  
 aggcaacagg attgatcatt cttttataga gcatatttgc caataaagct tttggaagcc 668  
 gg 670

<210> 5

<211> 152

<212> PRT

<213> Homo sapiens

<400> 5

Met Ala Asn Leu Glu Arg Thr Phe Ile Ala Ile Lys Pro Asp Gly Val  
 1 5 10 15  
 Gln Arg Gly Leu Val Gly Glu Ile Ile Lys Arg Phe Glu Gln Lys Gly  
 20 25 30  
 Phe Arg Leu Val Ala Met Lys Phe Leu Arg Ala Ser Glu Glu His Leu  
 35 40 45  
 Lys Gln His Tyr Ile Asp Leu Lys Asp Arg Pro Phe Phe Pro Gly Leu  
 50 55 60  
 Val Lys Tyr Met Asn Ser Gly Pro Val Val Ala Met Val Trp Glu Gly  
 65 70 75 80

Leu	Asn	Val	Val	Lys	Thr	Gly	Arg	Val	Met	Leu	Gly	Glu	Thr	Asn	Pro	
				85.					90							95
Ala	Asp	Ser	Lys	Pro	Gly	Thr	Ile	Arg	Gly	Asp	Phe	Cys	Ile	Gln	Val	
				100					105							110
Gly	Arg	Asn	Ile	Ile	His	Gly	Ser	Asp	Ser	Val	Lys	Ser	Ala	Glu	Lys	
				115					120							125
Glu	Ile	Ser	Leu	Trp	Phe	Lys	Pro	Glu	Glu	Leu	Val	Asp	Tyr	Lys	Ser	
				130					135							140
Cys	Ala	His	Asp	Trp	Val	Tyr	Glu									
145									150							